

**A MULTILOCATIONAL TRIAL OF FIFTEEN GENOTYPES OF
SHRUNKEN-2 SUPER SWEET MAIZE IN BENIN CITY**

BY

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**DEPARTMENT OF CROP SCIENCE
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BENIN CITY**

DECEMBER, 2022

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**A PROJECT REPORT SUBMITTED TO THE DEPARTMENT OF
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CERTIFICATION

This is to certify that this research was carried out by **Osarenren Bernard EFE**,
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(Head of Department)

Date

DEDICATION

This work is dedicated in God Almighty for his strength, provision and support.

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My sincere gratitude goes to God Almighty for his unfailing love grace and divine support upon my life.

I wish to express my wholehearted appreciation and profound gratitude to my supervisor Prof C.N.C. Nwaoguala for his selfless assistance, correction, guidance and fatherly advice throughout the period of this study to me sir you are a father.

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Am also thankful to my project colleagues Daje Blessing Esilokun, Anyin Chinagorom Florencia and Mr. Peter OKundaye for their corporation and to the entire graduating students of crop Science Department 2022 set. I say THANK YOU ALL AND MAY GOD BLESS YOU ALL

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ABSTRACT

The study seeks to examine the multi-locational trail of fifteen genotype of shrunken-2 super sweet maize in benin

city. The experiment was conducted at experimental farm with the premises of university of benin teaching hospital. Benin city, nigeria fifteen super sweet corn (maize) genotype “UISSH 1, UISSH 2, UISSH 3. UISSH4, UISSH 5, UISSH 6, UISSH 7, UISSH 8, UISSH 9, UISSH 10, UISSH 11, UISSH 12, UISSH 13, UISSH 14 and UISSH 15 varieties were evaluated in this experiment. The experiment was laid out in a randomized complete block design with three replications. The data collected was analyzed using Genstat version 12. Characters measured included Seedling emergence all 11 days, days to 50% tasseling, day to 50% silking, days to 50% pollen shedding. Ear height, plant height, number of, days to maturity, Number of cob, cob weight, husk cover, ear aspect and fresh ear yield. The effects of genotype (G) were found to be highly significant ($p<0:01$) days to 50% tasseling, days to 50% pollen shedding, Ear geight. The result of experiments showed that there was significant difference due to genotype effect in plant height, days to 50% tasseling, days to 50% pollen shedding, ear height, plant height and days to maturity. Genotype also affects days to Cob number, cob weight and fresh ear yield. The genotypes, UISSH3 was identified as one of the most promising for production Benin city although this variety can be improved for early emergence and better

CHAPTER ONE

INTRODUCTION

Multi-environment yield trials are essential in estimation of genotype by environment (GE) interaction and identification of superior genotypes in the final selection cycles;

Maize (*Zea mays* L...) is one of the most cultivated cereals in the world. Along with wheat and rice, it accounts for approximately 60% of the calories directly and indirectly ingested by humans (Cassman et al, 2003) in addition, it is one of the most studied species in breeding programmes and remains one of the main model species used in genetic studies (Walace et al.2024). Sweet corn (*Zea mays* L), considered a vegetable, is a special type of maize with particular characteristics, such as sweet taste, thin pericarp and endosperm with delicate texture, and high nutritional value (Kwiakowski and Clemente, 2007). It is destined exclusively for human consumption. In fresh form or in processed foods, whereas the straw can be used for silage after harvest (Teixeira et al., 2001). In Nigeria, sweet corn is grown on an estimated 36 million ha annually, with an average yield of 10-12 tons of ears. Ha-1 (Barvieri et al., 2005, Kwiatkowski and clemente, 2007), although recent data on the crop yield are not available.

The difference between sweet and common maize is that in the genome of the former, at least one of the eight genes that influence carbohydrate biosynthesis in the endosperm is mutant, preventing the conversion of carbohydrate to starch (Tracy et al, 2006, Qi et al. 2009). These genes comprise: shrunken-2 (sh2), brittle (bt), Amylose extender (ac), sugary enhancer (se), sugary (su), and Brittle-2 (bt2), "Dull" (du), and Waxy (wx), all monogenic and recessive. Among the maize cultivars with high sugar contents, the super-sweet corn cultivars stand out with even higher levels of carbohydrates than the sweet corn varieties (Oliveira Junior et al. 2006)

In plant breeding, the process of identifying genotypes with high yield potential and yield stability across environments is a fundamental activity (Djurovic et al., 2014) identification of stable genotypes by plant breeders is usually difficult due to the presence of genotype by environment interaction (GEI) (Beyene et al., 2012) GEI causes the relative ranking of genotype performance to change across environments and thereby affecting breeding progress (Nzuve et al., 2013). Due to GEI effect, genotypes with wide adaptation are rarely identified (Kwabena et al., 2019)

Environment fluctuation and interaction is also a major limitation for maize production and productivity especially in the tropics. Genotype by environment interaction (GEI) is the differential responses of different genotypes across a range of environments (Belo et al., 2019). In breeding, genotype x environment (G x E) cause many difficulties, while the environmental factors such as temperature soil affect the performance of genotypes. Genotype x environment (GE) interaction reduces the genetic progress in plant breeding programmes through minimizing the association between yield trials are essential in assessing of genotype by environment interaction (GEI) and identification of superior genotypes in the final selection cycles (Welu, 2015) Phenotypes are mixture of genotype (G) and environment ϵ components and interactions (G x E) between them. GxE interactions complicate process of selecting genotypes with superior performance. Multi-Local trials (MLTs) are widely used by plant breeders to evaluate the relative performance of genotypes for target environments (Adjebeng-Denquah,2017). Therefore the study was carried out to evaluate the multi-local trial of fifteen genotypes of shrunken-2 super sweet maize in Benin city as one of the trial locations

CHAPTER TWO

LITERATURE REVIEW

2.1 Maize production and uses

Maize (*Zea mays* L.), with a remarkable yield potential among the cereals, is the third most important grain crop after wheat and rice and accounts for 4.8% of the total cropped area and 3.5% of the value of the agricultural output (Ochse et al., 1996). Among the developing economies, it ranks first in Latin America and Africa (Dowswell et al., 1996). In the tropics, maize is grown in 66 countries and is of major economic significance in 61 of those countries (Paliwal, 2000).

In developing countries maize is generally used as food, while in the developed world, it is used widely as a major source of carbohydrate in animal feed and as industrial raw material. In sweeteners, there has been exponential growth in maize-based ethanol production, fuelled by rapid increases in world energy and petrol prices (FAO Food Outlook, 2006). Most people regard maize as a breakfast cereal. However, in a processed form it is also found as fuel (ethanol) and starch. Starch in turn undergoes enzymatic conversion into products such as sorbitol, dextrin, sorbic and lactic acid, and appears in household items such as beer, ice

cream, syrup, shoe polish, glue, fireworks, ink, batteries, mustard, cosmetics, aspirin and paint (Paliwal, 2000)

2.2 Varieties of maize

2.2.1 importance of early and extra-early maturing maize varieties

In Sub-Saharan Africa, in efforts to cope with rainfall risk, many small-scale farmers purposefully pursue multiple planting dates over extended periods of time in order to purposefully pursue multiple planting dates over extended periods of time in order to ensure that at least part of the crop is successful (Rorhrbach, 1998). According to Pswarayi and Vivek (2007), farmers grow early maturing maize varieties because such varieties provide early harvest to bridge the hunger period before harvest of a full season crop, and this especially important in areas where two growing seasons occur in a year. Farmers can produce an early maturing crop during the secondary, short season, enabling the planting of a full season maize crop or thoe crops in the following main season. Early maturing varieties offer flexivility in planting dates which enables (1) multiple planting in a season to spread the risk of loosing a single crop to mid season droughts (2) late planting during delayed onset of rainfall and (3)

avoidance of known terminal drought during the cropping season (Pswarayi and Vivek, 2007). Early maturing varieties are ideal for offseason plantings in drying riverbeds and are also suitable for intercropping as they provide less competition for moisture, light and nutrients than the late maturing varieties (CIMMYT, 2000). Using maize maturity to maintain grain yield in response to late season drought, in trials conducted in two locations over two seasons, Larson and Clegg (1999) found that use of well adapted early maturing hybrids could improve yield stability. They also found that an early maturing hybrid, Pioneer 3737, produced yield comparable to those of late maturing hybrids in all instances. Their results indicated that well adapted early maturing hybrids could produce yields comparable to late maturing hybrids in areas where late season water stress was prevalent. Kamara et al., (2006) evaluated three maize varieties that had been identified either as drought tolerant or as able to escape drought. The drought tolerant maize was evaluated on Farmers' fields for two years. Farmers selected extra-early maturing varieties, placing great emphasis on earliness of crop maturity rather than on yield.

According to the prediction of Zhang et al. (2009), the gap between requirement and productivity of maize would increase by 2020. The total production of maize may be enhanced by a variety of ways such as planting area expansion, soil improvement, fertilization and tillage optimization. However, the most effective and direct way is to breed varieties with high yielding potential and wide adaptability (Golbashy et al.,2010). Studies have proved that 52.9% of maize yield increment was attributed to varieties, and the rate of improvement was 89.1 kg/ha per year (ci et al.,2010; Li and Wang, 2009)

2.2.2 Sweet maize

Sweet corn (*Zea mays* L.) was first reported by European settlers in 1779 (Boyer and Shannon, 1983). It is one of the most popular vegetables in the United States and Canada and has observed enormous growth in consumption in most parts of Europe, Eaastern Asia, and Sout America (William et al.,1997, Tracy, 2001). Sweet corn has become extremely popular that when the word ‘corn’ is used, it is commonly assumed as sweet corn, even though field corn production is 50-60 times higher than that of sweet corn

2.2.3. Sweet maize and other maize

Sweet corn belongs to the same species of other types of corn (*Z mays*), such as popcorn and field corn, the grain that is most commonly produced in the world. The most distinguishing characteristic, when compared to any of the other corn types, is the result of naturally occurring recessive mutations that control the conversion of sugar into starch inside the endosperm (William et al., 2007). While the increased sugar content in the endosperm is what defines sweet corn, elite materials have historically been selected for the presence of additional traits that are relevant for the sweet corn market, such as aesthetics of ears, plants, and grain traits such as flavor, tenderness, and texture (Brewbaker and Martin, 2015). In the case of corn planted for the fresh market, most of the harvest is manual, which demands plants with low stature and biomass (Tracy, 2001). Furthermore, most sweet corn markets currently do not tolerate genetic engineering traits, therefore imposing additional selection pressures to enhance the plant tolerance to pests. Altogether, the considerable differences are highly noticeable between elite sweet corn hybrids and materials that are commercialized for feedstock and ethanol production. Sweet corn and field corn can be intercrossed, and this germplasm can be a good source of genetic diversity into a sweet corn breeding

programme (Tracy, 1990). However, all the starch-deficient genes that are commercially used in sweet corn are recessive. Therefore, Kernels of sweet corn must have two copies of each gene, for a kernel to express the sweetness trait (Mannering, 2008). Currently, the most popular and widely used genes are:

2.2.4 Sul (sugary 1)

Sugary 1 was the only commercially used sweet corn mutant after the discovery by East and Hayes (1911). *Su1* encodes a starch debranching isoamylase. The gene is expressed later in the starch biosynthesis pathway, and the mutant alleles reduces starch production while increasing the sugar content. *Su1* knock out alleles which results in around 15% of sugar at the immature milky phase of endosperm development (~20 days after pollination). Furthermore, sugary1 lines increase the concentration of phytoglycogen, providing a smooth and creamy texture to the grain (Creech, 1968). Upon the dry state, its kernels are translucent and have a glassy appearance. Regardless of its acclaimed taste, the use of sugary 1 mutants in the fresh market decreased due to the fast reduction in sugar content once the ears were harvested, thereby severely lowering the product's shelf life (Coe, 1988; Williams 1997).

2.2.5 Se (sugr enhancer)

Sugar enhancer is a feature that was discovered by phodes in 1970s and improves the sweet phenotype in sul backgrounds (ferguson, 2007). The gene cannot be used independently though since it doesn't have any effect on its own. The exact mechanism, enzyme. And role in the pathway for the se gene are still unknown. However, it is conventionally introduced into sul parents. Which results in an increase in sugar content by 10 to 25% in the hybrids (Gonzales et al.,2004). The se varieties have tender pericarp, lighter kernel color, and creamy texture like sugary lines. However, due to the higher sugar content, the hybrids also have a higher shelf life than sul lines.

2.2.6 Sh2 (shrunken2)

The Shruken 2 gene encodes the large subunit of the ADP – glucose pyrophosphorylase enzyme. This enzyme is the first committed step in starch biosynthesis. At present, this gene is the most widely mutant used commercially, as the knock-out allele inhibits starch synthesis at the beginning of the starch biosynthesis pathway which leads to ~35% of sugar accumulation and higher shelf life (Creechm 1968). The hybrids are generally referred to as

“supersweets”, and the dry seed has a shriveled texture and opaque appearance (Hallauer, 2000). The increased sugar content, however, comes with its negative consequences. The shrunken seeds have a significantly reduced amount of starch in the grain, which in turn creates germination problems (Wilson and Mohan, 2008). Hence, sh2 hybrids did not become commercially available until breeders were able to select materials that improved the germination rate (Tracy, 2001)

Table 2.1: commercially used genes in sweet corn breeding programmes, chromosome location to the maize genome, the type of enzyme produced and characteristics of the phenotype

Mutant type	Gene	Chromosome	Enzyme	Phenotype
Sugary 1	Su1	4	Starch debranching isoamylase	Translucent, wrinkled, bigorous seed, no shelf life
Sugary Enhancer1	Se1	2	Unknown	Creamy, tender color varies with the background slow drying, short shelf life
Shrunken 2	Sh2	3	ADP glucose pyrophosphorylase	Translucent, shriveled, sweet, crisp, long shelf-life low seed vigor
Synergistic		NA	NA	Crisp, vigorous seed, longer shelf life, mixed kernel types on the ear
Amylose extender 1	ae1	5	Starch branching enzyme	Tarnished, glassy, high amylose content
Brittle 1	Bt1	5	Starch granule-bound phosphor-oligosaccharide synthase	Angular often translucent, brittle, mature kernel collapsed
Brittle 2	bt2	4	ADP glucose pyrophosphorylase	Transparent, shriveled, sweet kernels collapse on drying becoming angular and brittle

Source: Boyer and Shannon, 2003; Coe et al., 1998, Lartrat and Pulam, 2007; William Tracy, 1997

2.3 Sweet maize Genotype and Environment Interaction

The differential of a genotype across environments is defined as the genotype (G) x environment E interaction GEI: Beyene et al.(2011) and Bernardo (2002) indicated that it is the rule in most quantitative characteristics. GEI makes it difficult to select the best performing and most stable genotypes. It is an important consideration in plant breeding programmes because it impedes progress from selection in any given environment (Yau, 1995). In breeding programmes, genotype stability for yield and agronomic performance is an important breeding objective. Previous research suggests that selection of superior genotypes for grain yield and agronomic traits in maize hybrid performance trials is impacted by GEI (Butron et al., 2004). The phenotype of an individual is determined by the effects of its genotype and the environment surrounding it. The effects of genotype and environment on phenotype may not be always independent. The phenotypic response to change in environment is not the same for all genotypes, the consequences of variation in phenotype depend upon the environment. Very often breeders encounter situations where the relative rankings of varieties change from location to location and/or from year to year

An understanding of environmental and genotypic causes of GEI is important at all stages of plant breeding, including ideotype design, parent selection based on traits, and selection based on yield (Jackson et al., 1998)). Understanding of the causes of GEI can be used to establish breeding objectives, to identify ideal test conditions, and to formulate recommendations for areas of optimal cultivar

adaptation. It can also help to reduce the cost of extensive genotype evaluation by eliminating unnecessary testing sites and by fine tuning the breeding programmes. The presence of a large GEI may necessitate establishment of additional testing sites, thus increasing the cost of developing commercially important varieties (Kang, 1996)

2.4 Significance of Genotype and Environment interaction

Factors that are of economic relevance may be related to complex or polygenic characteristics, and show a high influence of the environment. Because of this, in breeding programmes, various experiments are conducted in several locations to evaluate grain yield. In these experiments, changes in the relative performance of the genotype in different environments are usually observed (Kandus et al., 2010). The genotype by environment interaction is an important aspect in both, plant breeding programmes and the introduction of new maize hybrids. Deitos et al., (2006), indicated that genotype x environment interaction is important for plant breeding because it affects the genetic gain and recommendation and selection of cultivars with wide adaptability. On the other hand, different genotypes may have different performance in each region that can be capitalized to maximize productivity (Souza et al., 2008). Kang and Gorman (1989) indicated that, a significant GEI for a quantitative trait that GEI reduce the correlation between the genotype and the phenotype hindering the evaluation of the genetic potential of the cultivars

CHAPTER THREE

MATERIALS AND METHODS

3.1 Experimental Site

The experiment was conducted between July to October, 2021 at Experimental farm within the premises of University of Benin Teaching Hospital, Benin City, Nigeria. The location lies within latitude 6.39 N and longitude 5⁰61' and 5⁰36' E. The experimental site fall lies within the humid tropical climate. It is within the rainforest agroecological zone of Nigeria and has an annual rainfall of 1762-2300 mm per annum with high relative humidity. The daily temperatures ranged from 28 and 41⁰C as the minimum and maximum , respectively. The site was dominated by the sensitive plant (*Mimosa padica*), Guinea grass (*Panicum maximum*) and other creeping weeds prior to the planting of Maize. The soil type was characterized by well drained sandy loam soil and a moderately flat topography

3.2 Genotype used

The fifteen super sweet corn (maize) genotypes “UISSH 1, UISSH 2, UISSH 3, UISSH 4, UISSH 5, UISSH 6, UISSH 7, UISSH 8, UISSH 9, UISSH 10, UISSH 11, UISSH 12, UISSH 13, UISSH 14 and UISSH 15 varieties were evaluated in this experiment. The maize varieties were developed by Prof. Victor A. Adetimrin of Department of Agronomy, University of Ibadan. The supersweet corn genotypes were undergoing a multilocational trial prior to formal release as

commercial sweetcorn varieties. Benin city was one of the multilocations for the trial.

3.3 Experimental design and treatments

The experiment was laid out in a randomized complete block design with three replications. Each plot size was 5, long with 0.5 m between plots and 0.5 , between blocks were marked out. Each replicate had 15 plots and total of 45 plots made up the experimental site which occupied an area of 78m².

3.4 Cultural practice

The land was cleared with cutlass, hoe and spade after the site was marked out into blocks and plots using wooden pegs, twines and mallet. The planting depth was 1.5cm and Placement orientation was horizontal. The crop was rain-fed/watered through the growing season. Weeding was done as at when appropriate. Fertilizer was applied. Insecticides was applied.

3.5 Plant Parameters Collection

3.5.1 Plant height

The height was measured from the soil level to the point where the flag leaf emerges from the plant using a measuring tapr. The height of five (5) plants per treatment was measured and the unit expressed in centimeters (cm) at 9 weeks after planting.

3.5.2 Ear Height

The height was measured from the base of the plant to the node bearing the uppermost ear. The height of 5 plants per treatment was measured and the unit expressed in centimeter at 9 weeks after planting.

3.5.3 Weight of cob

The matured ripe maize fruits per plants were harvested by hand picking, weighed using a weighing scale and recorded

3.5.4 Number of ears per plot

After hand picking, the total number of cob harvested was counted

3.5.5 Weight of ears per plot

Total weight of cobs harvested with the husks intact were weighed

3.5.6 Husk cover

This was measured based on the tightness or exposure of kernels on a scale of 1-5

3.5.7 Number of cobs per plot in

This was weighed with husk removed from each ear. Only ears of 200 kernels was assessed

3.8 Statistical Analysis

Plant parameters measured were subjected to analysis of Variance (ANOVA) using GENSTAT 12th Edition. Significance means were separate using fisher's protected least significant differences (LED) test.

CHAPTER FOUR

4.1 Measurement of variation due to genotype

The mean values indicating the differences in agronomic trait of the 15 genotype of super sweet hybrid maize the 15 maize are presented in Table 1. The Analysis of variance super shows significant difference in all the seven (7) agronomic trait measured. There was very highly significant difference ($P < 0.001$) for days to 50% tasseling, days to 50% pollen shedding and ear height. Seedling emergence after eleven days, days to 50% silking, plant height and day's to maturity was significant ($P < 0.05$).

4.2 Mean value of agronomic trait evaluated

The mean values for all the grown traits tested are presented in Table 2

4.2.1 Seedling emergence

Seedling emergence was allowed to linger for 11 days because 5 days, a good number of the genotype had not fully germinated until after 11 days and from all indications most of the genotype were not significantly difference ($p > 0.05$) from one another. UISSH2 had the hightes (98.33%) emergence after 11 days while UISSH12 had the lowest (73.33%) emergence.

Table 4.1: Mean square value Agronomic traits of super sweet hybrid maize genotypes evaluated in Benin City.

Source of variation	Degree of freedom	Seedling emergence at 11 days	Days to 50% tasseling	Days to 50% silking	Days to 50% pollen shedding	Ear height (cm)	Plant height (cm)	Days to maturity
Replication	2	3.27	29.62	30.82	22.16	211.53	432.0	30.82
Genotype	14	6.25*	13.17***	2.75*	9.66***	237.40***	703.7*	10.26*
Residual	28	2.39	2.69	3.73	2.37	45.59	105.2	3.73

Table 4.2: Mean value Agronomic traits of super sweet hybrid maize genotypes evaluated in Benin City.

Genotype	Seeding emergence at 11 days	Days To 50% Tesselling	Days to 50% silking	Days to 50% pollen shedding	Ear height (cm)	Plant height (cm)	Days to maturity
UISSH1	90.00 ^{ab}	55.67 ^{abcde}	61.67 ^{bcde}	57.33 ^{def}	60.73 ^a	151.3 ^a	82.67 ^{bcde}
UISSH2	98.33 ^a	54.33 ^{defg}	61.00 ^{de}	57.33 ^{def}	54.87 ^{abc}	143.5 ^{ab}	82.00 ^{de}
UISSH3	90.00 ^{ab}	54.00 ^{defg}	61.33 ^{cde}	57.33 ^{def}	34.87 ^{ef}	116.1 ^{defg}	82.33 ^{cde}
UISSH4	91.67 ^{ab}	58.33 ^a	64.00 ^{abcd}	60.67 ^a	55.53 ^{ab}	140.5 ^{abc}	85.0 ^{abcd}
UISSH5	95.00 ^{ab}	54.00 ^{defg}	61.67 ^{bcde}	58.0 ^{bcde}	39.20 ^{def}	114.9 ^{defg}	82.67 ^{bcde}
UISSH6	88.33 ^{abc}	55.33 ^{bcdef}	61.00 ^{de}	58.33 ^{abcde}	40.87 ^{def}	113.5 ^{fg}	82.00 ^{de}
UISSH7	95.00 ^{ab}	56.67 ^{abcd}	62.67 ^{abcde}	60.00 ^{abc}	34.87 ^{ef}	106.2 ^g	83.67 ^{abcde}
UISSH8	96.67 ^{ab}	56.67 ^{abcd}	64.67 ^{ab}	60.33 ^{ab}	55.00 ^{ab}	146.6 ^{ab}	85.67 ^{ab}
UISSH9	95.00 ^{ab}	57.33 ^{abc}	64.33 ^{abc}	59.67 ^{abcd}	29.93 ^f	102.2 ^g	85.33 ^{abc}
UISSH10	76.67 ^{cd}	53.67 ^{efg}	60.33 ^e	56.33 ^{ef}	42.33 ^{de}	125.3 ^{cdef}	81.33 ^e
UISSH11	96.67 ^{ab}	52.00 ^g	60.00 ^e	55.33 ^f	38.60 ^{def}	114.7 ^{efg}	81.00 ^e
UISSH12	73.33 ^d	58.00 ^{ab}	65.33 ^a	60.33 ^{ab}	48.20 ^{bcd}	131.9 ^{bcd}	86.33 ^a
UISSH13	90.00 ^{ab}	55.00 ^{cdef}	61.67 ^{bcde}	57.67 ^{cdef}	43.67 ^{cde}	133.9 ^{bc}	82.00 ^{de}
UISSH14	85.00 ^{bcd}	51.67 ^g	59.67 ^e	56.67 ^{ef}	42.60 ^{de}	130.9 ^{bcde}	80.67 ^e
UISSH15	93.33 ^{ab}	52.67 ^{fg}	60.00 ^e	55.33 ^f	37.67 ^{def}	115.2 ^{defg}	81.00 ^e
Standard errors of differences	1.26	1.34	1.58	1.26	5.51	8.37	1.58
Cumulative variance	8.5	3.0	3.1	2.7	15.3	8.2	2.3

4.2.2 50% days to tasseling

Genotype UISSH14 was the earliest to 50% tasseling at while UISSH14 was the latest at 58.33 days, average of 51.67 days

Various sweet hybrid maize. Although genotype UISSH2, USSH3 and UISSH5 shows no significant difference. Also UISSH7 UISSH8 shows no significant difference. There was a highly ($p < 0.001$) significance difference in days to 50% tasseling and the various sweet corn hybrid, difference in tasseling percentage might be to the genetic make-up of the varieties and adaptation to the environment.

4.2.3 50% days to silking

Days to 50% silking was earliest (65.33) in UISSH13 while days to 50% silking was latest (59.67) in UISSH14. There was a ($P < 0.001$) significance difference among the various maize genotype evaluated.

4.2.4 50% days to pollen

Days to 50% pollen shedding was earliest (60.67) in UISSH4 while days to 50% pollen was latest (55.33) in UISSH15. There was a high ($P < 0.001$) significance difference in the various genotype to 50% pollen shedding.

4.2.5 Ear height

Ear height from 34.87 – 60.73. ear height was height (60.73cm) in UISSH1 while the lowest (34.87cm) in UISSH3. There was highly ($P < 0.001$) significant difference in ear height of the different maize genotypes.

4.2.6 Plant height

Plant height was highest (151.3cm) in UISSH1 while plant height was lowest (102.2cm) in UISSH9). There was a ($P < 0.001$) significant difference among the various genotype of super sweet maize.

4.2.7 Days to maturity

Different genotype of super sweet maize shows different days to maturity. Days to maturity took between 80-60 days for the different genotype of the maize variety evaluated. The days to maturity was earliest in UISSH14 (80.67cm) while days to maturity was latest in UISSH12 (86.33). there was ($P < 0.001$) difference across the various genotype of super sweet maize.

4.3 mean square value of fresh ear yield and their component of super sweet hybrid maize

The mean square value for fresh ear yield and other component of super sweet maize presented in table 3. The analysis of variance indicated that there were ($P < 0.001$) highly significant difference on the number of cob per plot as well as fresh ear yield. Cob weight was significant at ($P < 0.005$) while Husk cover and Ear aspect were not significant at ($P > 0.05$).

Table 4.3: Mean square value of fresh ear yield and other components of super sweet hybrid maize.

Source	Fresh ear yield	Degree of freedom	Number of cob per plot	Cob weight	Husk cover	Ear aspect
Replication	523	2	60.20	1.23	0.27	0.33
Genotype	4211**	14	22.77**	0.63*	0.86	0.68
Residual	1376	28	7.49	0.23	0.55	0.56

4.4 Fresh Ear yield and other components of super sweet hybrid maize

4.4.1 Number of cob

The mean values for number of cob due to genotype are shown in table 4. Cob with less than 200 seeds were not considered. From the data presented from the result of the study, it was observed that there was a ($P < 0.001$) significant difference in most of the parameters measured. Number of cobs was highest (17.67cm) in UISSH3 while number of cob was lowest (3.33cm) in Uissh12. This wide variation might be due to the genetic potential of the different genotype. There was a significant difference in number of cob among the various maize genotype'

4.4.2 cob weight

Cob weight ranged from 0.38cm-1.72cm. the cob weight was highest (1.72cm) in UISSH11 while cob weight was lowest (0.38cm) in UISSH9. There was a ($P < 0.001$) high significance difference in cob weight among the different genotype of super sweet maize. The difference in cob weight might be attributed to the genetic makeup of the different genotype.

Table 4: Mean value of fresh ear yield and other components of super sweet hybrid maize.

Genotype	Fresh ear yield (t/ha)	Number of cob	Cob weight (kg)	Husk cover (1-9)	Ear aspect (1-9)
UISSH1	6.72 ^{bcd}	12.00 ^a	1.52 ^{abc}	2.31	3.33
UISSH2	8.21 ^{ab}	11.67 ^a	1.82 ^a	3.00	2.77
UISSH3	7.92 ^{abc}	17.67 ^{abc}	1.13 ^{abcd}	4.10	3.67
UISSH4	6.54 ^{bcde}	6.33 ^{bc}	0.82 ^{cd}	3.00	3.33
UISSH5	4.89 ^e	4.33 ^c	0.40 ^d	4.00	4.00
UISSH6	7.31 ^{abcd}	6.00 ^{bc}	0.80 ^{cd}	3.33	3.00
UISSH7	8.82 ^a	6.00 ^{bc}	1.03 ^{abcd}	2.67	2.67
UISSH8	7.56 ^{abcd}	7.00 ^{bc}	1.02 ^{abcd}	3.00	3.00
UISSH9	6.37 ^{cde}	3.33 ^c	0.38 ^d	3.67	3.33
UISSH10	7.59 ^{abcd}	6.00 ^{bc}	0.97 ^{bcd}	3.67	2.33
UISSH11	8.72 ^a	10.33 ^{ab}	1.72 ^{ab}	2.67	3.00
UISSH12	6.37 ^{cde}	3.33 ^c	0.40 ^d	3.33	3.33
UISSH13	6.44 ^{bcde}	4.33 ^c	0.50 ^d	3.67	3.67
UISSH14	7.21 ^{abcd}	5.00 ^c	0.68 ^d	4.00	3.00
UISSH15	6.06 ^{de}	7.67 ^{abc}	0.87 ^{cd}	3.67	4.00
Standard errors of differences	30.29	2.23	0.39	0.61	0.61
Cumulative variance	14.8	40.6	51.3	22.3	23.1

4.4.3 Husk cover and ear aspect

The husk cover ranged from 2.31cm-4.10cm. the husk cover was highest (4.10cm) in UISSH3 while the husk cover lowest (2.31cm) in UISSH1. There was no significant difference in husk cover among the 15 different genotype used in the study. The Earaspect was highest (4.00cm) in UISSH5 and (4.00cm) in UISSH15 while the ear aspect was lowest (2.33cm) in UISSH10.

4.4.4 Fresh ear yield

The Fresh ear yield ranged from 6.06cm- 8.82cm. The fresh ear yield highest (8.82cm) in UISSH8 while the fresh ear yield was lowest (60.06cm) in UISSH15. There was a ($P < 0.001$) high significant diffence across the various maize genotype.

CHAPTER FIVE

5.1 Discussion

The study showed that there were highly significant differences among (days to 50% tasseling, days to 50% pollen shedding, Ear height), although, the effect of genotype had to significant influence on traits like husk Cover and ear aspect. The difference in the evaluated traits of the genotypes, indicates variability in the inherent makeup which is peculiar to each genotype and the fact that they may have originated from different parental background. The result of the finding agrees with Bello et al. (2012) who noted that performance of genotypes both between and within different group for grain yield, plant height, days to maturity to the diversity of the genotype and their differences for these characters. Cultivar performance is a function of the genotype and the production environment where it grows.

The study showed that USISSH12 shows earlier days to emergence when compared to the other genotypes. Studies has shown that different genotype shows different day to emergence and day to maturity. This wide variation that exist might be due to the genic potential of the different genotypes hence some

genotype tend to emerge and mature earlier while other do not (Hallauer and Miranda. 2008). The various causes have been described as sources of GEL in Sub-saharan Africa maize growing environments; for instance temperature, rainfall, drought, length of growing season, sub soil pH and socio-economic (sub-optimal input application) (Banziger et al., 2002). Rainfall also plays a significant role in the stimulation of plant to speed up the process of maturity. The early days to maturity can also be attributed to favourable environmental conditions which gives USISSHI2 an opportunity to express their efficient water use. Number of days to 50% tasseling, 50% silking, and pollen shedding were highly significant. This observation can be substantiated with the findings of Jaimin et al. (2004).

This implies that the later the number of days it takes a cultivar to attain, tasseling and/or silking the lower the grain yield obtain. Days to silking is an important character that can be used in ranking genotype for their suitability as genotype for cultivation during marginal rain periods such as late planting season in the region. Earliness to silking allows short growth duration and maturity and these constitute important attributes to drought escape which often make early

maturing varieties adapted to late season moisture stress than later maturing ones (Olaoye and Omueti, 2006).

Plant height and ear height are other important traits for breeding new varieties of maize for dry matter production as well as increased grain yield as a result of reduction in root and stalk lodging. A very high position is believed to increase maize susceptibility to root and stalk lodging. From the result of the study UISSH12 are usually relatively shorter with low ear position (Bello et al., 2012). These can serve as a great source of alleles for breeding programmes in developing new cultivars that are resistant to stalk lodging. Accordingly, the number of Cobs was highest (17.67) in UISSH3 while number of cob was lowest (3.33) in UI5SH12. This wide variation might be due to the genetic potential of the different genotypes. Tannenc et al. (2013).

5.2 Conclusion

From this study Genotype of the 15 super sweet maize hybrids evaluated was found to be significant for most of the parameter measured. The presence of large genetic variability for the parameter measured indicated that, good progress can

be made in selecting for maize yield. Although, variability among genotypes. Genotype were found to contribute greatly to the variations in hybrid's performance. This indicates that, unpredictable environmental conditions are one of the major players in selecting superior and widely adapted maize varieties under Nigeria condition. Hence, hybrids selected should be specifically adapted to the different environments. The presence of significant genotypic mean squares for days to silking, days to emergence, plant height, ear height, number of stalk and root lodging justified the use of the Multi-trait Selection method to identify the best genotypes for the production. Also genotype that are early to attain 50% silking will as well bring about increase in yield and cope drought stress especially in the late planting season.

5.3 Recommendations

It can be recommended that:

- Further testing can be carried out on UISSH3 since it mature early so as to escape the prolonged moisture stress.

- The genotype should serve as potential source of unique favourable alleles which could be used by breeders for developing high yielding genotype that can adapt better and produce a higher economic yield.

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